

SEQUENCE LISTING

<110> Hayward, Nicholas K.
Weber, Gunther
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Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
SAME

<130> DAVIES

<140> 08/765,588

<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 649

<212> DNA

<213> Nucleotide Sequence of VEGF165

<220>

<221> CDS

<222> (17)..(589)

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gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
15 20 25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
30 35 40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
45 50 55 60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
65 70 75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg	292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg	340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag	388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa	436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa	484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln	
145 150 155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc	532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys	
160 165 170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag	580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys	
175 180 185	
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg	629
Pro Arg Arg	
190	
gaaccagatc tctcaccagg	649

<210> 2

<211> 191

<212> PRT

<213> Nucleotide Sequence of VEGF165

<400> 2

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		20						25					30		

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 3

<211> 1094

<212> DNA

<213> Nucleotide Sequence of SOM175

<220>

<221> CDS

<222> (3)..(623)

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 1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143

Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125

aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
 130 135 140

cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
 145 150 155

ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
 160 165 170 175

gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
 180 185 190

gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
 Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

tagagctcaa ccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683

agactcagca ggggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
 ggctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattctaca actggctctt 983
 cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4
 <211> 207
 <212> PRT
 <213> Nucleotide Sequence of SOM175

<400> 4

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			20					25					30		
Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln
		35					40					45			
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val
		50				55					60				
Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
65					70				75					80	
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
			85						90					95	
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
		100						105					110		
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
		115					120					125			
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	Arg
	130					135					140				
Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro
145					150					155					160
Ser	Pro	Ala	Asp	Ile	Thr	His	Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	Ala

	165		170		175										
His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Ala
	180						185					190			
Ala	Ala	Ala	Asp	Ala	Ala	Ala	Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
	195						200					205			

<210> 5
 <211> 993
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>
 <221> CDS
 <222> (3)..(566)

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 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 7
<211> 858
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
<221> CDS
<222> (3)..(431)

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30

<210> 8
 <211> 143
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

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 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
 130 135 140

<210> 9
 <211> 910
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
 <221> CDS
 <222> (3)..(305)

<400> 9
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 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgtg tgaagccaga 335
 Gln Val Arg Met Gln Thr
 100
 cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395
 ccccgagca cctccccag ctgacatcac ccatcccact ccagccccag gccctctgc 455
 ccacgctgca ccagcacca ccagcgcct gacccccgga cctgccgctg ccgctgccga 515
 cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575
 tgccggaagc tgcgaaggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635
 aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755
 ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815
 gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct cttcc

910

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<211> 101

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exon 4

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Thr
100

<210> 11

<211> 42

<212> DNA

<213> Oligonucleotide

<400> 11

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42

<210> 12

<211> 42

<212> DNA

<213> Oligonucleotide

<400> 12

agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13

<211> 38

<212> DNA

[illegible]

38

40

236

1

225

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gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40					45					50			
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
		55					60					65				
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggc	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
	70					75					80					
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
85					90					95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
				105					110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120					125					130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
		135				140						145				
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
	150					155					160					
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
165					170					175					180	
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
 165 170 175
 Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
 180 185 190
 Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
 195 200 205

<210> 18
 <211> 188
 <212> PRT
 <213> mVRF167

<400> 18
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
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 20 25 30
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
 50 55 60
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro
 130 135 140
 Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160
 Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys
 180 185

<210> 19
 <211> 188

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
 50 55 60

Ser Ile Ala Lys Gly Gly Ala
 65 70

<210> 21
 <211> 71
 <212> PRT
 <213> hVRF186

<400> 21
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Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
 20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
 35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser
 50 55 60

Ser Val Ala Lys Gly Gly Ala
 65 70

<210> 22
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 <212> PRT
 <213> mVEGF188

<400> 22
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
 20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
 35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
 50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
 85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
 100 105 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
 115 120 125
 Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
 130 135 140
 Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
 145 150 155 160
 Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
 165 170 175
 Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
 180 185 190
 Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
 195 200 205
 Cys Asp Lys Pro Arg Arg
 210